

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 12:54:54 ; Search time 108 Seconds  
(without alignments)  
5594.172 Million cell updates/sec

Title: US-09-931-232-2

Perfect score: 850

Sequence: 1 atggtgagcaaggaggagga.....taggatcaatgttagatgc 850

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	100.0	850	3	US-09-062-102-2
2	850	100.0	850	3	US-09-364-946-2
3	718.6	84.5	761	4	US-09-869-588-25
4	718.6	84.5	5069	4	US-09-393-483A-1
5	718.6	84.5	5069	4	US-09-393-483A-2
6	718.6	84.5	7015	4	US-09-770-315-1
7	718.6	84.5	9423	4	US-09-377-066-6
8	718	84.5	4397	4	US-09-503-799-1
9	717.4	84.4	720	3	US-09-172-063-11
10	717.4	84.4	720	4	US-09-316-919-12
11	717.4	84.4	720	4	US-09-602-641-11
12	717.4	84.4	720	4	US-09-920-822-1
13	717.4	84.4	720	4	US-09-316-920A-12
14	717.4	84.4	972	3	US-09-172-063-29
15	717.4	84.4	972	4	US-09-602-641-29
16	717.4	84.4	1095	3	US-09-085-305-5
17	717.4	84.4	1140	4	US-09-417-197-128
18	717.4	84.4	1635	4	US-09-417-197-112
19	717.4	84.4	1815	4	US-09-417-197-58
20	717.4	84.4	1821	4	US-09-417-197-64
21	717.4	84.4	1893	4	US-09-417-197-62
22	717.4	84.4	1929	2	US-08-818-253-1
23	717.4	84.4	1929	2	US-08-818-253-5
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25	717.4	84.4	1929	3	US-08-818-252-5
26	717.4	84.4	2043	4	US-09-800-170-47
27	717.4	84.4	2157	4	US-09-417-197-74

28 717.4 84.4 2181 4 US-09-417-197-70 Sequence 70, Appl  
29 717.4 84.4 2394 4 US-09-417-197-140 Sequence 140, App  
30 717.4 84.4 2397 4 US-09-417-197-60 Sequence 76, Appl  
31 717.4 84.4 2511 4 US-09-417-197-60 Sequence 60, Appl  
32 717.4 84.4 2562 4 US-09-417-197-118 Sequence 118, App  
33 717.4 84.4 2592 3 US-09-591-025-8 Sequence 8, Appl  
34 717.4 84.4 2592 4 US-09-894-927B-8 Sequence 8, Appl  
35 717.4 84.4 2598 4 US-09-417-197-110 Sequence 110, App  
36 717.4 84.4 2799 4 US-09-417-197-136 Sequence 136, App  
37 717.4 84.4 2913 4 US-09-417-197-66 Sequence 66, Appl  
38 717.4 84.4 2991 4 US-09-417-197-122 Sequence 122, App  
39 717.4 84.4 3138 4 US-09-417-197-78 Sequence 78, Appl  
40 717.4 84.4 3546 4 US-09-796-575-4 Sequence 132, App  
41 717.4 84.4 4748 4 US-09-796-575-4 Sequence 4, Appl  
42 717.4 84.4 4992 4 US-09-796-575-5 Sequence 5, Appl  
43 717.4 84.4 8614 3 US-09-208-827-5 Sequence 5, Appl  
44 717.4 84.4 8614 4 US-10-043-074-5 Sequence 5, Appl  
45 717.4 84.4 9687 3 US-09-133-944-2 Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-09-062-102-2  
; Sequence 2, Application US/09062102  
; Patent No. 6130313  
; GENERAL INFORMATION:  
; APPLICANT: Kain, Steve  
; APPLICANT: Li, Xianqiang  
; TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods  
; TITLE OF INVENTION: of Use  
; FILE REFERENCE: D6100  
; CURRENT APPLICATION NUMBER: US/09/062,102  
; CURRENT FILING DATE: 1998-04-17  
; EARLIER APPLICATION NUMBER: US 60/060,855  
; EARLIER FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 3  
; SEQ ID NO 2  
; LENGTH: 850  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: DNA sequence which encodes the EGFP-MODC422-461  
; OTHER INFORMATION: fusion protein.  
US-09-062-102-2

Query Match 100.0%; Score 850; DB 3; Length 850;  
Best Local Similarity 100.0%; Pred. No. 1.6e-168;  
Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGTGAGCAAGGCGAGGAGCTGTTCCACGGGGTGTGCCATCTCTGCTGAGCTGCAC 60  
Db 1 ATGTGAGCAAGGCGAGGAGCTGTTCCACGGGGTGTGCCATCTCTGCTGAGCTGCAC 60  
Qy 61 GGGACGTAACCGCCCAAGTTTTCAGCGTGTCCGGGAGGCGGAGGCGGATGCCACCTAC 120  
Db 61 GGGACGTAACCGCCCAAGTTTTCAGCGTGTCCGGGAGGCGGAGGCGGATGCCACCTAC 120  
Qy 121 GGCAGCTGACCTGAGTTTCATCTGCACCGGAGGAGTGCCTGCGCTGCCGCCACC 180  
Db 121 GGCAGCTGACCTGAGTTTCATCTGCACCGGAGGAGTGCCTGCGCTGCCGCCACC 180  
Qy 181 CTGCTGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 240  
Db 181 CTGCTGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 240  
Qy 241 CAGCAGCTTCTTAAAGTCCGCGCATGCCGAAGGTTACGTCAGGAGGCGGAGGCGGAGG 300  
Db 241 CAGCAGCTTCTTAAAGTCCGCGCATGCCGAAGGTTACGTCAGGAGGCGGAGGCGGAGG 300  
Qy 301 TTCAAGGAGCGAGGCAACTACAGAGCCCGCGGAGGTTGAGGTTGAGGCGGAGGCGGAG 360



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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: mutant green
US-09-869-588-25

Query Match      84.5%; Score 718.6; DB 4; Length 761;
Best Local Similarity 98.8%; Pred. No. 3.7e-141;
Matches 724; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTGTAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 60
Db 20 ATGTGTAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 79

QY 61 GGCAGCGTAAACGGCCCAAGTTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 120
Db 80 GGCAGCGTAAACGGCCCAAGTTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 139

QY 121 GGCAGCGTAAACGGCCCAAGTTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 180
Db 140 GGCAGCGTAAACGGCCCAAGTTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 199

QY 181 CTCGTGACCAACCTGACCTACCGGTGCAAGTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 240
Db 200 CTCGTGACCAACCTGACCTACCGGTGCAAGTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 259

QY 241 CAGCAGCACTTCTTCAAGTCGCGCATGCCCGAAGGCTACGTCAGGAGCGCACCCTTC 300
Db 260 CAGCAGCACTTCTTCAAGTCGCGCATGCCCGAAGGCTACGTCAGGAGCGCACCCTTC 319

QY 301 TTCAGGACGACGCAACTCAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCTG 360
Db 320 TTCAGGACGACGCAACTCAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCTG 379

QY 361 GTCAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGCAACATCTCTGGGGC 420
Db 380 GTCAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGCAACATCTCTGGGGC 439

QY 421 AAGCTGGAGTAACTCAACAGCCCAACAGCTTATATCATGGCCGACAGCAGAAGAAC 480
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QY 481 GGCATCAAGGTGAATTCAGATCCGCCCAACATCGAGGACGCGTGCAGCTGCC 540
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QY 541 GACCACCTACCAAGCAACACCCCATCGCGACGCGCCCGTGTGTGCTGCCCGCAACCC 600
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QY 601 TACCTGAGCAACCGAGTCCGCGCTGAGCAAGACCCCAAGAGAGCGCGATCAGTGGTC 660
Db 620 TACCTGAGCAACCGAGTCCGCGCTGAGCAAGACCCCAAGAGAGCGCGATCAGTGGTC 679

QY 661 CTCGTGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGACGAGCTGTACAAGAG 720
Db 680 CTCGTGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGACGAGCTGTACAAGAG 739

QY 721 CTTAGCCATGGCT 733
Db 740 AGCGGCGCGACT 752
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## RESULT 4

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US-09-393-483A-1
; Sequence 1, Application US/09393483A
; Patent No. 6689936
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Amano, Satoshi
; APPLICANT: Kishimoto, Jiro
; APPLICANT: Nishiyama, Toshio
```

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; APPLICANT: Ehama, Ritsuko
; TITLE OF INVENTION: METHODS FOR EVALUATING A COMPOUND FOR
; FILE OF INVENTION: ITS EFFECT ON SKIN
; FILE REFERENCE: 10287-054001
; CURRENT APPLICATION NUMBER: US/09/393,483A
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 09/070,436
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/069,945
; PRIOR FILING DATE: 1997-12-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-393-483A-1
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Query Match 84.5%; Score 718.6; DB 4; Length 5069;

Best Local Similarity 98.8%; Pred. No. 5.4e-141;

Matches 724; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 1 ATGTGTAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 60
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QY 61 GGCAGCGTAAACGGCCCAAGTTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 120
Db 1075 GGCAGCGTAAACGGCCCAAGTTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 1134

QY 121 GGCAGCGTAAACGGCCCAAGTTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 180
Db 1135 GGCAGCGTAAACGGCCCAAGTTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 1194

QY 181 CTCGTGACCAACCTGACCTACCGGTGCAAGTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 240
Db 1195 CTCGTGACCAACCTGACCTACCGGTGCAAGTTCAGCGGTGTCCGGCGAGGGCGGATGCCACCTAC 1254

QY 241 CAGCAGCACTTCTTCAAGTCGCGCATGCCCGAAGGCTACGTCAGGAGCGCACCCTTC 300
Db 1255 CAGCAGCACTTCTTCAAGTCGCGCATGCCCGAAGGCTACGTCAGGAGCGCACCCTTC 1314

QY 301 TTCAGGACGACGCAACTCAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCTG 360
Db 1315 TTCAGGACGACGCAACTCAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCTG 1374

QY 361 GTCAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGCAACATCTCTGGGGC 420
Db 1375 GTCAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGCAACATCTCTGGGGC 1434

QY 421 AAGCTGGAGTAACTCAACAGCCCAACAGCTTATATCATGGCCGACAGCAGAAGAAC 480
Db 1435 AAGCTGGAGTAACTCAACAGCCCAACAGCTTATATCATGGCCGACAGCAGAAGAAC 1494

QY 481 GGCATCAAGGTGAATTCAGATCCGCCCAACATCGAGGACGCGTGCAGCTGCC 540
Db 1495 GGCATCAAGGTGAATTCAGATCCGCCCAACATCGAGGACGCGTGCAGCTGCC 1554

QY 541 GACCACCTACCAAGCAACACCCCATCGCGACGCGCCCGTGTGTGCTGCCCGCAACCC 600
Db 1555 GACCACCTACCAAGCAACACCCCATCGCGACGCGCCCGTGTGTGCTGCCCGCAACCC 1614

QY 601 TACCTGAGCAACCGAGTCCGCGCTGAGCAAGACCCCAAGAGAGCGCGATCAGTGGTC 660
Db 1615 TACCTGAGCAACCGAGTCCGCGCTGAGCAAGACCCCAAGAGAGCGCGATCAGTGGTC 1674

QY 661 CTCGTGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGACGAGCTGTACAAGAG 720
Db 1675 CTCGTGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGACGAGCTGTACAAGAG 1734

QY 721 CTTAGCCATGGCT 733
Db 1735 AGCGGCGCGACT 1747
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RESULT 5  
 US-09-393-483A-2/c  
 ; Sequence 2, Application US/09393483A  
 ; Patent No. 6889936  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burgeson, Robert  
 ; APPLICANT: Amano, Satoshi  
 ; APPLICANT: Kishimoto, Jiro  
 ; APPLICANT: Nishiyama, Toshio  
 ; APPLICANT: Ehama, Ritsuko  
 ; TITLE OF INVENTION: METHODS FOR EVALUATING A COMPOUND FOR  
 ; FILE OF INVENTION: ITS EFFECT ON SKIN  
 ; CURRENT APPLICATION NUMBER: US/09/393,483A  
 ; CURRENT FILING DATE: 1999-09-10  
 ; PRIOR FILING DATE: 1998-04-30  
 ; PRIOR APPLICATION NUMBER: 60/069,945  
 ; PRIOR FILING DATE: 1997-12-17  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 5069  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-393-483A-2  
  
 Query Match 84.5%; Score 718.6; DB 4; Length 5069;  
 Best Local Similarity 98.8%; Pred. No. 5.4e-141;  
 Matches 724; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
 QY 1 ATGGTGAGCAAGGGGAGAGAGTGTTCACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 60  
 DB 4055 ATGGTGAGCAAGGGGAGAGAGTGTTCACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 3996  
  
 QY 61 GCGCAGCTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120  
 DB 3995 GCGCAGCTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 3936  
  
 QY 121 GCGCAGCTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 180  
 DB 3935 GCGCAGCTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 3876  
  
 QY 181 CTCGTGACCAACCTGACCTACGCGGTGCAAGTGTTCAGCGGCTACCCCGACCAATGAAG 240  
 DB 3875 CTCGTGACCAACCTGACCTACGCGGTGCAAGTGTTCAGCGGCTACCCCGACCAATGAAG 3816  
  
 QY 241 CAGCAGCACTTCTTCAAGTCCGCGATGCGCGGAGGCTAGTCCAGGAGCGCACCTCTTC 300  
 DB 3815 CAGCAGCACTTCTTCAAGTCCGCGATGCGCGGAGGCTAGTCCAGGAGCGCACCTCTTC 3756  
  
 QY 301 TTCAAGGAGCAGCGCAACTACAGACCGCGCGAGGTGAAGTTCCGAGGCGCACACCTTG 360  
 DB 3755 TTCAAGGAGCAGCGCAACTACAGACCGCGCGAGGTGAAGTTCCGAGGCGCACACCTTG 3696  
  
 QY 361 GTGAACCGCATCGAGCTGAAGGSCATCGACTTCAAGGAGGAGCGGCAACATCTCTGGGSCAC 420  
 DB 3695 GTGAACCGCATCGAGCTGAAGGSCATCGACTTCAAGGAGGAGCGGCAACATCTCTGGGSCAC 3636  
  
 QY 421 AAGCTGGAGTACAACTACAGCCCAACAGTCTATATATGCGCGCAAGCAGCAGAGAAC 480  
 DB 3635 AAGCTGGAGTACAACTACAGCCCAACAGTCTATATATGCGCGCAAGCAGCAGAGAAC 3576  
  
 QY 481 GGCATCAAGGTGAATTTCAAGATCCCGCAACATCGAGGAGCGGCGAGTGCAGCTCGCC 540  
 DB 3575 GGCATCAAGGTGAATTTCAAGATCCCGCAACATCGAGGAGCGGCGAGTGCAGCTCGCC 3516  
  
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 DB 3515 GACCATTACGAGCAGAACCCCGCATCGGCGAGCGGCCCGTGTGTGTCGCCGACACCCAC 3456

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 DB 3455 TACCTGAGCAACCCAGTCCGCGCTGAGCAAGAGAGCCCAAGAGAGCGGCGATCACATGGTC 3396  
  
 QY 661 CTGCTGGAGTTCTGTCACCGCGCGCGGATCACTCTCGCATGAGCAGAGCTGTACAAGAG 720  
 DB 3395 CTGCTGGAGTTCTGTCACCGCGCGCGGATCACTCTCGCATGAGCAGAGCTGTACAAGTAA 3336  
  
 QY 721 CTAGCCATGGCT 733  
 DB 3335 AGCGGCGCGACT 3323  
  
 RESULT 6  
 US-09-770-315-1  
 ; Sequence 1, Application US/09770315  
 ; Patent No. 6429001  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chiron Corporation  
 ; TITLE OF INVENTION: Recombinant AAV Packaging Systems  
 ; FILE REFERENCE: 20263-501  
 ; CURRENT APPLICATION NUMBER: US/09/770,315  
 ; CURRENT FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: US 60/178,536  
 ; PRIOR FILING DATE: 2000-01-26  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 7015  
 ; TYPE: DNA  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: recombinant DNA  
 US-09-770-315-1  
  
 Query Match 84.5%; Score 718.6; DB 4; Length 7015;  
 Best Local Similarity 98.8%; Pred. No. 5.7e-141;  
 Matches 724; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
 QY 1 ATGGTGAGCAAGGGGAGAGAGTGTTCACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 60  
 DB 3171 ATGGTGAGCAAGGGGAGAGAGTGTTCACCGGGGTGGTCCCATCTCTGTCGAGCTGGAC 3230  
  
 QY 61 GCGCAGCTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120  
 DB 3231 GCGCAGCTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 3290  
  
 QY 121 GCGCAGCTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 180  
 DB 3291 GCGCAGCTAAAGCGGCACAAAGTTACGCGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 3350  
  
 QY 181 CTCGTGACCAACCTGACCTACGCGGTGCAAGTGTTCAGCGGCTACCCCGACCAATGAAG 240  
 DB 3351 CTCGTGACCAACCTGACCTACGCGGTGCAAGTGTTCAGCGGCTACCCCGACCAATGAAG 3410  
  
 QY 241 CAGCAGCACTTCTTCAAGTCCGCGATGCGCGGAGGCTAGTCCAGGAGCGCACCTCTTC 300  
 DB 3411 CAGCAGCACTTCTTCAAGTCCGCGATGCGCGGAGGCTAGTCCAGGAGCGCACCTCTTC 3470  
  
 QY 301 TTCAAGGAGCAGCGCAACTACAGACCGCGCGAGGTGAAGTTCCAGGCGCACACCTTG 360  
 DB 3471 TTCAAGGAGCAGCGCAACTACAGACCGCGCGAGGTGAAGTTCCAGGCGCACACCTTG 3530  
  
 QY 361 GTGAACCGCATCGAGCTGAAGGSCATCGACTTCAAGGAGGAGCGGCAACATCTCTGGGSCAC 420  
 DB 3531 GTGAACCGCATCGAGCTGAAGGSCATCGACTTCAAGGAGGAGCGGCAACATCTCTGGGSCAC 3590  
  
 QY 421 AAGCTGGAGTACAACTACAGCCCAACAGTCTATATATGCGCGCAAGCAGCAGAGAAC 480  
 DB 3591 AAGCTGGAGTACAACTACAGCCCAACAGTCTATATATGCGCGCAAGCAGCAGAGAAC 3650  
  
 QY 481 GGCATCAAGGTGAATTTCAAGATCCCGCAACATCGAGGAGCGGCGAGTGCAGCTCGCC 540

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Db 3651 GGCATCAGGTGAATTCAGATCGGCCACAACATCGAGGACGGCAGCGTGCAGCTGCC 3710
Qy 541 GACCACTACCGAGAGAACACCCCATCGGCGACGCGCCCGTGTCTGCTGCCCGACAACCCAC 600
Db 3711 GACCACTACCGAGAGAACACCCCATCGGCGACGCGCCCGTGTCTGCTGCCCGACAACCCAC 3770
Qy 601 TACCTGAGCACCAGTCCGCTCGAGCAAGAACCCCAACGAGAGCGGATCAGATGTC 660
Db 3771 TACCTGAGCACCAGTCCGCTCGAGCAAGAACCCCAACGAGAGCGGATCAGATGTC 3830
Qy 661 CTGCTGGAGTTCTGTAACCGCCCGCGGATCACTCTCGGCATGGACGAGCTGTACAAGAAG 720
Db 3831 CTGCTGGAGTTCTGTAACCGCCCGCGGATCACTCTCGGCATGGAGAGCTGTACAAGTAA 3890
Qy 721 CTTAGCCATGGCT 733
Db 3891 AGCGCGCGGACT 3903

RESULT 7
US-09-377-066-6
; Sequence 6, Application US/09377066A
; Patent No. 6773914
; GENERAL INFORMATION:
; APPLICANT: Handler, Alfred M.
; TITLE OF INVENTION: PiggyBac Transfection System
; FILE REFERENCE: 0194.98
; CURRENT APPLICATION NUMBER: US/09/377,066A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 6
; LENGTH: 9423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: pB(PuB-nls-BGFP)#257
US-09-377-066-6

Query Match 84.5%; Score 718.6; DB 4; Length 9423;
Best Local Similarity 98.8%; Pred. No. 6e-141;
Matches 724; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGTCCTCTGCTGAGCTGGAC 60
Db 5377 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGTCCTCTGCTGAGCTGGAC 5436
Qy 61 GCGAGCTAAACGGCCACACAGTTTCAGCGTGTCCGCGAGGGCGAGGGCGATGCCACCTAC 120
Db 5437 GCGAGCTAAACGGCCACACAGTTTCAGCGTGTCCGCGAGGGCGAGGGCGATGCCACCTAC 5496
Qy 121 GGCAAGCTGACCTGAGTTCATCTGTCACCAACCGGCAAGCTGCGCTGCGCTGCGCCACC 180
Db 5497 GGCAAGCTGACCTGAGTTCATCTGTCACCAACCGGCAAGCTGCGCTGCGCTGCGCCACC 5556
Qy 181 CTGCTGACCAACCTGACCTACGGGTGCGTGTTCAGCGCTACCCCGACCAATGAAG 240
Db 5557 CTGCTGACCAACCTGACCTACGGGTGCGTGTTCAGCGCTACCCCGACCAATGAAG 5616
Qy 241 CAGCAGACTTCTTCAAGTCCCGCATGCCCGAAGGCTACGTCAGGAGCGCAATCTTC 300
Db 5617 CAGCAGACTTCTTCAAGTCCCGCATGCCCGAAGGCTACGTCAGGAGCGCAATCTTC 5676
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Db 5737 GTGAAACCGCATCAGCTGAAGGGGATCGATCTTAAGGAGGACGGCAACATCTTGGGGCAC 5796
Qy 421 AAGCTGGAGTACACTACACAGCCCAACAGTCTATATATATGCGCCGACAGCAGAGAAC 480
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Db 5797 AAGCTGGAGTACAACTACACAGCCCAACACGCTCTATATCATGGCCGACAAGCAGAAGAAC 5856
Qy 481 GGCAATCAAGGTGAATTCAGATCCGCCACAACATCGAGGACGGCAGCTGCAGCTGCC 540
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Qy 541 GACCACTACCGAGAGAACACCCCATCGGCGACGCGCCCGTGTCTGCTGCCCGACAACCCAC 600
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Db 6037 CTGCTGGAGTTCTGTAACCGCCCGCGGATCACTCTCGGCATGGAGAGCTGTACAAGTAA 6096
Qy 721 CTTAGCCATGGCT 733
Db 6097 AGCGCGCGGACT 6109

RESULT 8
US-09-503-799-1
; Sequence 1, Application US/09503799
; Patent No. 6451563
; GENERAL INFORMATION:
; APPLICANT: Wittig, Burghardt
; APPLICANT: Junghans, Claas
; APPLICANT: Schroff, Matthias
; TITLE OF INVENTION: METHOD FOR MAKING LINEAR, COVALENTLY CLOSED DNA CONSTRUCTS
; FILE REFERENCE: NHL-NP-21
; CURRENT APPLICATION NUMBER: US/09/503,799
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4397
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pUC 19 derivative, comprising a coding sequence for the modified
; OTHER INFORMATION: enhanced green fluorescence protein from aquaeora victoria under
; OTHER INFORMATION: control of cmv-promoter
US-09-503-799-1

Query Match 84.5%; Score 718; DB 4; Length 4397;
Best Local Similarity 100.0%; Pred. No. 7e-141;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGTCCTCTGCTGAGCTGGAC 60
Db 3073 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGTCCTCTGCTGAGCTGGAC 3132
Qy 61 GCGAGCTAAACGGCCACACAGTTTCAGCGTGTCCGCGAGGGCGAGGGCGATGCCACCTAC 120
Db 3133 GCGAGCTAAACGGCCACACAGTTTCAGCGTGTCCGCGAGGGCGAGGGCGATGCCACCTAC 3192
Qy 121 GGCAAGCTGACCTGAGTTCATCTGTCACCAACCGGCAAGCTGCGCTGCGCTGCGCCACC 180
Db 3193 GGCAAGCTGACCTGAGTTCATCTGTCACCAACCGGCAAGCTGCGCTGCGCTGCGCCACC 3252
Qy 181 CTGCTGACCAACCTGACCTACGGGTGCGTGTTCAGCGCTACCCCGACCAATGAAG 240
Db 3253 CTGCTGACCAACCTGACCTACGGGTGCGTGTTCAGCGCTACCCCGACCAATGAAG 3312
Qy 241 CAGCAGACTTCTTCAAGTCCCGCATGCCCGAAGGCTACGTCAGAGGAGCGCAACATCTTC 300
Db 3313 CAGCAGACTTCTTCAAGTCCCGCATGCCCGAAGGCTACGTCAGAGGAGCGCAACATCTTC 3372
Qy 301 TTCAAGGACGACGGCACTACAAGACCGCGCGAGGTGAAGTTTCAGAGGCGCACACCCCTG 360
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Db 3373 TTCAAGGACGCGCACTAAGACCCGCGCGAGGTGAAGTTTCGAGGGGACACCCCTG 3432  
Qy 361 GTGAACCCCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTCGGGGCAC 420  
Db 3433 GTGAACCCCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTCGGGGCAC 3492  
Qy 421 AAGCTGGAGTAACTAACAAGCCACAAAGCTTATATCATGGCCGCAAGCAGAAGAAC 480  
Db 3493 AAGCTGGAGTAACTAACAAGCCACAAAGCTTATATCATGGCCGCAAGCAGAAGAAC 3552  
Qy 481 GGCATCAAGGTGAAGTCAAGATCCGCCACACATCGAGGAGCGGAGCGTGCAGCTCGCC 540  
Db 3553 GGCATCAAGGTGAAGTCAAGATCCGCCACACATCGAGGAGCGGAGCGTGCAGCTCGCC 3612  
Qy 541 GACCACTACCAAGCAGAAACACCCCATCGCGAGCGGCCCGCTGCTGTCGCCGCAACACCAC 600  
Db 3613 GACCACTACCAAGCAGAAACACCCCATCGCGAGCGGCCCGCTGCTGTCGCCGCAACACCAC 3672  
Qy 601 TACCTGAGCACCGAGTCCGCCCTGAGCAAAAGACCCCAAGAGAGGGCGATCACATGGTC 660  
Db 3673 TACCTGAGCACCGAGTCCGCCCTGAGCAAAAGACCCCAAGAGAGGGCGATCACATGGTC 3732  
Qy 661 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGCATGAGCGAGCTGTACAAGA 718  
Db 3733 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGCATGAGCGAGCTGTACAAGA 3790

## RESULT 9

US-09-172-063-11  
; Sequence 11, Application US/09172063  
; Patent No. 6150176  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; APPLICANT: Llopis, Juan  
; APPLICANT: Wachter, Rebekka M.  
; APPLICANT: Remington, S. James  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE  
; FILE REFERENCE: 07257/071001  
; CURRENT APPLICATION NUMBER: US/09/172,063  
; EARLIER FILING DATE: 1998-10-13  
; EARLIER APPLICATION NUMBER: 09/094,359  
; EARLIER FILING DATE: 1998-06-09  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Aequorea victoria  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (0)..(0)  
; OTHER INFORMATION: EGFP  
US-09-172-063-11

Query Match 84.4%; Score 717.4; DB 3; Length 720;  
Best Local Similarity 99.9%; Pred. No. 6.6e-141;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGTGAGCAAGGGGAGAGAGCTGTTACCGGGGTGGTCCCATCTGTTGTCGAGCTGGAC 60  
Db 1 ATGGTGAGCAAGGGGAGAGAGCTGTTACCGGGGTGGTCCCATCTGTTGTCGAGCTGGAC 60  
Qy 61 GGCAGCTAAACGGCCACAAAGTTTCAGCGTGTCCGGGAGGGCGAGGGCGATGCCACTAC 120  
Db 61 GGCAGCTAAACGGCCACAAAGTTTCAGCGTGTCCGGGAGGGCGAGGGCGATGCCACTAC 120  
Qy 121 GGCAAGCTGACCTGAAGTTTCATCTGCAACCGGCAAGTGCCTGTCCTGGCCACC 180  
Db 121 GGCAAGCTGACCTGAAGTTTCATCTGCAACCGGCAAGTGCCTGTCCTGGCCACC 180

Qy 181 CTCGTGACCAACCTGACCTAGCGGTGAGTGTCTTTCAGCGGTACCCCGACACATGAAG 240  
Db 181 CTCGTGACCAACCTGACCTAGCGGTGAGTGTCTTTCAGCGGTACCCCGACACATGAAG 240  
Qy 241 CAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTAGTTCAGGAGCGACCATCTTTC 300  
Db 241 CAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTAGTTCAGGAGCGACCATCTTTC 300  
Qy 301 TTCAAGGAGCGAGCAACTACAGACCCCGCGCGAGGTGAAGTTTCGAGGGGACACCCCTG 360  
Db 301 TTCAAGGAGCGAGCAACTACAGACCCCGCGCGAGGTGAAGTTTCGAGGGGACACCCCTG 360  
Qy 361 GTGAACCCCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTCGGGGCAC 420  
Db 361 GTGAACCCCATCGAGCTGAAGGGCATCGACTTCAAGAGGAGCGGCAACATCTCGGGGCAC 420  
Qy 421 AAGCTGGAGTAACTAACAAGCCACAAAGCTTATATCATGGCCGCAAGCAGAAGAAC 480  
Db 421 AAGCTGGAGTAACTAACAAGCCACAAAGCTTATATCATGGCCGCAAGCAGAAGAAC 480  
Qy 481 GGCATCAAGGTGAAGTCAAGATCCGCCACACATCGAGGAGCGGAGCGTGCAGCTCGCC 540  
Db 481 GGCATCAAGGTGAAGTCAAGATCCGCCACACATCGAGGAGCGGAGCGTGCAGCTCGCC 540  
Qy 541 GACCACTACCAAGCAGAAACACCCCATCGCGAGCGGCCCGCTGCTGTCGCCGCAACACCAC 600  
Db 541 GACCACTACCAAGCAGAAACACCCCATCGCGAGCGGCCCGCTGCTGTCGCCGCAACACCAC 600  
Qy 601 TACCTGAGCACCGAGTCCGCCCTGAGCAAAAGACCCCAAGAGAGGGCGATCACATGGTC 660  
Db 601 TACCTGAGCACCGAGTCCGCCCTGAGCAAAAGACCCCAAGAGAGGGCGATCACATGGTC 660  
Qy 661 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGCATGAGCGAGCTGTACAAGA 719  
Db 661 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGCATGAGCGAGCTGTACAAGA 719

## RESULT 10

US-09-316-919-12  
; Sequence 12, Application US/09316919  
; Patent No. 6469154  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Baird, Geoffrey  
; TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS  
; FILE REFERENCE: 07257/073001  
; CURRENT APPLICATION NUMBER: US/09/316,919  
; CURRENT FILING DATE: 1999-05-21  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Aequorea victoria  
US-09-316-919-12

Query Match 84.4%; Score 717.4; DB 4; Length 720;  
Best Local Similarity 99.9%; Pred. No. 6.6e-141;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGTGAGCAAGGGGAGAGAGCTGTTACCGGGGTGGTCCCATCTGTTGTCGAGCTGGAC 60  
Db 1 ATGGTGAGCAAGGGGAGAGAGCTGTTACCGGGGTGGTCCCATCTGTTGTCGAGCTGGAC 60  
Qy 61 GGCAGCTAAACGGCCACAAAGTTTCAGCGTGTCCGGGAGGGCGAGGGCGATGCCACTAC 120  
Db 61 GGCAGCTAAACGGCCACAAAGTTTCAGCGTGTCCGGGAGGGCGAGGGCGATGCCACTAC 120  
Qy 121 GGCAAGCTGACCTGAAGTTTCATCTGCAACCGGCAAGTGCCTGTCCTGGCCACC 180  
Db 121 GGCAAGCTGACCTGAAGTTTCATCTGCAACCGGCAAGTGCCTGTCCTGGCCACC 180  
Qy 181 CTCGTGACCAACCTGACCTAGCGGTGAGTGTCTTTCAGCGGTACCCCGACACATGAAG 240

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Db 181 CTCGTGACCACTTACCGGCTGAGTCTTACCGCGTACCCCGACCAATGAAG 240
QY 241 CAGCAGACTTCTTCAAGTCGCGCTGCGCGAGGCTAGCTCCAGGAGCGACCATCTTC 300
Db 241 CAGCAGACTTCTTCAAGTCGCGCTGCGCGAGGCTAGCTCCAGGAGCGACCATCTTC 300
QY 301 TTCAGGAGCGGCGCAACTAGAGACCGCGCGAGGTTGAAGTTGAGGGCGACACCTTG 360
Db 301 TTCAGGAGCGGCGCAACTAGAGACCGCGCGAGGTTGAAGTTGAGGGCGACACCTTG 360
QY 361 GTGAACCGCATCGAGTGAAGGCGCTGCACTTCAAGGAGGAGCGCAACATCTCTGGGCGAC 420
Db 361 GTGAACCGCATCGAGTGAAGGCGCTGCACTTCAAGGAGGAGCGCAACATCTCTGGGCGAC 420
QY 421 AAGCTGGAGTCAACTCAACAGCGCACCAACGCTCTATATCATGCGCGCGCAAGCAGAGAAC 480
Db 421 AAGCTGGAGTCAACTCAACAGCGCACCAACGCTCTATATCATGCGCGCGCAAGCAGAGAAC 480
QY 481 GGCATCAGGTTGAACTTCAAGATCCGCGCACACATCGAGGAGCGGAGCTCGCTCGCC 540
Db 481 GGCATCAGGTTGAACTTCAAGATCCGCGCACACATCGAGGAGCGGAGCTCGCTCGCC 540
QY 541 GACCACTACAGCAGCAACACCGCCATCGCGCGAGCGCGCGCTGCTGCGCGCGCAACACAC 600
Db 541 GACCACTACAGCAGCAACACCGCCATCGCGCGAGCGCGCGCTGCTGCGCGCGCAACACAC 600
QY 601 TACCTGAGCAGCGAGTCCGCGCTGAGCAAGAGACCGCGCGAGTCAACAGTGC 660
Db 601 TACCTGAGCAGCGAGTCCGCGCTGAGCAAGAGACCGCGCGAGTCAACAGTGC 660
QY 661 CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGCATGGAGCTGTACAAGAA 719
Db 661 CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGCATGGAGCTGTACAAGAA 719
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## RESULT 11

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US-09-602-641-11
; Sequence 11, Application US/09602641
; Patent No. 6608189
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Llopis, Juan
; APPLICANT: Wachter, Rebekka M.
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: MEASURING THE PH OF A BIOLOGICAL SAMPLE
; CURRENT APPLICATION NUMBER: US/09/602,641
; PRIOR FILING DATE: 2000-06-22
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: EGFP
US-09-602-641-11
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Query Match 84.4%; Score 717.4; DB 4; Length 720;
Best Local Similarity 99.9%; Pred. No. 6.6e-141;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGTAGCAAGGCGGAGGAGCTGTTTCAACCGGGTGGTGGCCATCTCTGGTGGAGCTGGAC 60
Db 1 ATGTGTAGCAAGGCGGAGGAGCTGTTTCAACCGGGTGGTGGCCATCTCTGGTGGAGCTGGAC 60
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QY 61 GCGCAGTAACCGGCCAACAGTTTCAAGCGTGTCCGCGAGGCGGAGCGGATGCCACTTAC 120
Db 61 GCGCAGTAACCGGCCAACAGTTTCAAGCGTGTCCGCGAGGCGGAGCGGATGCCACTTAC 120
QY 121 GSCAAGCTGACCTCAAGTTTCACTTGCACACCGGCAAGCTGCCGTGCCCTGGCCCCACC 180
Db 121 GSCAAGCTGACCTCAAGTTTCACTTGCACACCGGCAAGCTGCCGTGCCCTGGCCCCACC 180
QY 181 CTCGTGACCACTGACCTTACCGCGTGCAGTCTTTCAGCCGCTACCCCGACCAATGAAG 240
Db 181 CTCGTGACCACTGACCTTACCGCGTGCAGTCTTTCAGCCGCTACCCCGACCAATGAAG 240
QY 241 CAGCAGACTTCTTCAAGTCGCGCTGCGCGAGGCTAGCTCCAGGAGCGACCATCTTC 300
Db 241 CAGCAGACTTCTTCAAGTCGCGCTGCGCGAGGCTAGCTCCAGGAGCGACCATCTTC 300
QY 301 TTCAGGAGCGGCGCAACTAGAGACCGCGCGAGGTTGAAGTTGAGGGCGACACCTTG 360
Db 301 TTCAGGAGCGGCGCAACTAGAGACCGCGCGAGGTTGAAGTTGAGGGCGACACCTTG 360
QY 361 GTGAACCGCATCGAGTGAAGGCGCTGCACTTCAAGGAGGAGCGCAACATCTCTGGGCGAC 420
Db 361 GTGAACCGCATCGAGTGAAGGCGCTGCACTTCAAGGAGGAGCGCAACATCTCTGGGCGAC 420
QY 421 AAGCTGGAGTCAACTCAACAGCGCACCAACGCTCTATATCATGCGCGCGCAAGCAGAGAAC 480
Db 421 AAGCTGGAGTCAACTCAACAGCGCACCAACGCTCTATATCATGCGCGCGCAAGCAGAGAAC 480
QY 481 GGCATCAGGTTGAACTTCAAGATCCGCGCACACATCGAGGAGCGGAGCTCGCTCGCC 540
Db 481 GGCATCAGGTTGAACTTCAAGATCCGCGCACACATCGAGGAGCGGAGCTCGCTCGCC 540
QY 541 GACCACTACAGCAGCAACACCGCCATCGCGCGAGCGCGCGCTGCTGCGCGCGCAACACAC 600
Db 541 GACCACTACAGCAGCAACACCGCCATCGCGCGAGCGCGCGCTGCTGCGCGCGCAACACAC 600
QY 601 TACCTGAGCAGCGAGTCCGCGCTGAGCAAGAGACCGCGCGAGTCAACAGTGC 660
Db 601 TACCTGAGCAGCGAGTCCGCGCTGAGCAAGAGACCGCGCGAGTCAACAGTGC 660
QY 661 CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGCATGGAGCTGTACAAGAA 719
Db 661 CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGCATGGAGCTGTACAAGAA 719
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## RESULT 12

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US-09-920-922-1
; Sequence 1, Application US/09920922
; Patent No. 6673610
; GENERAL INFORMATION:
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Sawano, Asako
; TITLE OF INVENTION: METHOD FOR MUTAGENESIS
; FILE REFERENCE: 11283-012001
; CURRENT APPLICATION NUMBER: US/09/920,922
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(717)
US-09-920-922-1
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Query Match 84.4%; Score 717.4; DB 4; Length 720;
Best Local Similarity 99.9%; Pred. No. 6.6e-141;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY	1	ATGTTGACAAAGGGCGAGAGCTGTTTCAACGGGGTGGTCCCATCCTGTTGAGCTGGAC	60
Db	1	ATGGTGACAAAGGGCGAGAGCTGTTTCAACGGGGTGGTGGCCATCCTGTTGAGCTGGAC	60
QY	61	GGGACGTAACGGGCCAAAGTTCAGCGTGTCCGGCGAGGGCGAGGGGATGCCACCTAC	120
Db	61	GGGACGTAACGGGCCAAAGTTTACGCTGTCCGGCGAGGGCGAGGGGATGCCACCTAC	120
QY	121	GGCAAGCTGACCCCTGAAGTTTCATCTGCACCAACGGCAAGCTCCCGGTGCCCTGGCCACC	180
Db	121	GGCAAGCTGACCCCTGAAGTTTCATCTGCACCAACGGCAAGCTCCCGGTGCCCTGGCCACC	180
QY	181	CTCGTGACCAACCTGACCTACCGGGTGAGTGCCTTTCAGCCGCTACCCCGACACATGAAG	240
Db	181	CTCGTGACCAACCTGACCTACCGGGTGAGTGCCTTTCAGCCGCTACCCCGACACATGAAG	240
QY	241	CAGCACGACTTCTTCAAGTCGCCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCATCTTTC	300
Db	241	CAGCACGACTTCTTCAAGTCGCCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCATCTTTC	300
QY	301	TTCAAGGACGACGGCAACTTAAGACCCCGCGCGAGGTGAAGTTTGAGGGGACACCCCTG	360
Db	301	TTCAAGGACGACGGCAACTTACAAAGACCCCGCGCGAGGTGAAGTTTGAGGGGACACCCCTG	360
QY	361	GTGAACCGCATCGAGTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGTGGGGCAC	420
Db	361	GTGAACCGCATCGAGTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGTGGGGCAC	420
QY	421	AAGCTGGAGTCAAACTTACAACGCCAACACGCTCTATATCATGCGCCGACAAAGCAGAAAC	480
Db	421	AAGCTGGAGTCAAACTTACAACGCCAACACGCTCTATATCATGCGCCGACAAAGCAGAAAC	480
QY	481	GGCATCAAGGTGAACCTTCAAGATCCGCCAACATCGAGGACGGCAGCGTGCAGCTCGCC	540
Db	481	GGCATCAAGGTGAACCTTCAAGATCCGCCAACATCGAGGACGGCAGCGTGCAGCTCGCC	540
QY	541	GACCACTACGACGAAACACCCCATCGGCGACGGCCCCGTGCTGTGCCCGCAACACCAC	600
Db	541	GACCACTACGACGAAACACCCCATCGGCGACGGCCCCGTGCTGTGCCCGCAACACCAC	600
QY	601	TACCTGAGCACCCAGTCCGCGCTGACGAAGACCCCAACGAGNAGCGCGATCACATGGTC	660
Db	601	TACCTGAGCACCCAGTCCGCGCTGAGCAAGACCCCAACGAGNAGCGCGATCACATGGTC	660
QY	661	CTGCTGGAGTTCGTGACCGCCCGCGGATCACTCTCGGCATGGACGAGCTGTACAAGAA	719
Db	661	CTGCTGGAGTTCGTGACCGCCCGCGGATCACTCTCGGCATGGACGAGCTGTACAAGTA	719

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RESULT 13
US-09-316-920A-12
; Sequence 12, Application US/09316920A
; Patent No. 6699687
;
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGEN1470
; CURRENT APPLICATION NUMBER: US/09/316,920A
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
US-09-316-920A-12

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	RESULT	14	
US-09-172	; Sequenc	:	
	; Patent	:	
	; GENERAL	:	
	; APPLIC	:	
	; APPLIC	:	
	; APPLIC	:	
	; APPLIC	:	
	; TITLE	:	
	; FILE R	:	
	; CURREN	:	
	; EARLIE	:	
	; EARLIE	:	
	; NUMBER	:	
	; SOFTWARE	:	
	: SEQ ID	:	
	: LENGTH	:	
	: TYPE	:	
	: ORGAN	:	
	: FEATU	:	



; NAME/KEY: misc feature  
; LOCATION: (0)---(0)  
; OTHER INFORMATION: GT-EGFP  
US-09-172-063-29

Query Match 84.4%; Score 717.4; DB 3; Length 972;  
Best Local Similarity 99.9%; Pred. No. 6.9e-141;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCTGGTCAAGCTGGAC	60
Db	253	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCTGGTCAAGCTGGAC	312
QY	61	GGCGAGCTAAACGGCCACAAAGTTCAAGCTGTCGGGAGGGGAGGGCGATGCCACCTAC	120
Db	313	GGCGAGCTAAACGGCCACAAAGTTCAAGCTGTCGGGAGGGGAGGGCGATGCCACCTAC	372
QY	121	GGCAAGCTGACCTGAAAGTTCACTGTCACACCGCAAGCTGCCGTGCCCTGGGCCACC	180
Db	373	GGCAAGCTGACCTGAAAGTTCACTGTCACACCGCAAGCTGCCGTGCCCTGGGCCACC	432
QY	181	CTCGTGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG	240
Db	433	CTCGTGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG	492
QY	241	CAGCAGCACTTCTTCAAGTCCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCG	300
Db	493	CAGCAGCACTTCTTCAAGTCCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCG	552
QY	301	TTCAGGACGACGGCAACTCAAGACCGCGCGAGGTGAAGTTCCGAGGGCGACACCTG	360
Db	553	TTCAGGACGACGGCAACTCAAGACCGCGCGAGGTGAAGTTCCGAGGGCGACACCTG	612
QY	361	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGG	420
Db	613	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGG	672
QY	421	AAGCTGGAGTCAACTCAACAGCCACAACTGCTATATCATGTCGCGCAAGCAGAGAAC	480
Db	673	AAGCTGGAGTCAACTCAACAGCCACAACTGCTATATCATGTCGCGCAAGCAGAGAAC	732
QY	481	GGCATCAAGGTGAATTCAGATCCGCCCAACATCCGAGGACGGCAGGTGCGCTCGCC	540
Db	733	GGCATCAAGGTGAATTCAGATCCGCCCAACATCCGAGGACGGCAGGTGCGCTCGCC	792
QY	541	GACCACTACAGAGCAACACCCCATCGGCGAGCGCCCGCTGCTGCTGCCCGACAAACC	600
Db	793	GACCACTACAGAGCAACACCCCATCGGCGAGCGCCCGCTGCTGCTGCCCGACAAACC	852
QY	601	TACCTGAGCACCAGTCCGCGCTGAGCAAGACCCCAAGAGGAGCGGATCATGCTGTC	660
Db	853	TACCTGAGCACCAGTCCGCGCTGAGCAAGACCCCAAGAGGAGCGGATCATGCTGTC	912
QY	661	CTGCTGGAGTTCTGTCAGCGCGCGGGATCACTCTCGGCATGGAGCGAGCTGTACAAGAA	719
Db	913	CTGCTGGAGTTCTGTCAGCGCGCGGGATCACTCTCGGCATGGAGCGAGCTGTACAAGTA	971

## RESULT 15

US-09-602-641-29  
; Sequence 29, Application US/09602641  
; Patent No. 6608189  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; APPLICANT: Llopis, Juan  
; APPLICANT: Wachter, Rebekka M.  
; APPLICANT: Remington, S. James  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE  
; FILE REFERENCE: 07257/071001  
; CURRENT APPLICATION NUMBER: US/09/602,641  
; CURRENT FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 09/172,063  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 972  
; TYPE: DNA  
; ORGANISM: Aequorea victoria  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (0)---(0)  
; OTHER INFORMATION: GT-EGFP  
US-09-602-641-29

Query Match 84.4%; Score 717.4; DB 4; Length 972;  
Best Local Similarity 99.9%; Pred. No. 6.9e-141;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCTGGTCAAGCTGGAC	60
Db	253	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCTGGTCAAGCTGGAC	312
QY	61	GGCGAGCTAAACGGCCACAAAGTTCAAGCTGTCGGGAGGGGAGGGCGATGCCACCTAC	120
Db	313	GGCGAGCTAAACGGCCACAAAGTTCAAGCTGTCGGGAGGGGAGGGCGATGCCACCTAC	372
QY	121	GGCAAGCTGACCTGAAAGTTCACTGTCACACCGCAAGCTGCCGTGCCCTGGGCCACC	180
Db	373	GGCAAGCTGACCTGAAAGTTCACTGTCACACCGCAAGCTGCCGTGCCCTGGGCCACC	432
QY	181	CTCGTGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG	240
Db	433	CTCGTGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG	492
QY	241	CAGCAGCACTTCTTCAAGTCCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCG	300
Db	493	CAGCAGCACTTCTTCAAGTCCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCG	552
QY	301	TTCAGGACGACGGCAACTCAAGACCGCGCGAGGTGAAGTTCCGAGGGCGACACCTG	360
Db	553	TTCAGGACGACGGCAACTCAAGACCGCGCGAGGTGAAGTTCCGAGGGCGACACCTG	612
QY	361	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGG	420
Db	613	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGGG	672
QY	421	AAGCTGGAGTCAACTCAACAGCCACAACTGCTATATCATGTCGCGCAAGCAGAGAAC	480
Db	673	AAGCTGGAGTCAACTCAACAGCCACAACTGCTATATCATGTCGCGCAAGCAGAGAAC	732
QY	481	GGCATCAAGGTGAATTCAGATCCGCCCAACATCCGAGGACGGCAGGTGCGCTCGCC	540
Db	733	GGCATCAAGGTGAATTCAGATCCGCCCAACATCCGAGGACGGCAGGTGCGCTCGCC	792
QY	541	GACCACTACAGAGCAACACCCCATCGGCGAGCGCCCGCTGCTGCTGCCCGACAAACC	600
Db	793	GACCACTACAGAGCAACACCCCATCGGCGAGCGCCCGCTGCTGCTGCCCGACAAACC	852
QY	601	TACCTGAGCACCAGTCCGCGCTGAGCAAGACCCCAAGAGGAGCGGATCATGCTGTC	660
Db	853	TACCTGAGCACCAGTCCGCGCTGAGCAAGACCCCAAGAGGAGCGGATCATGCTGTC	912
QY	661	CTGCTGGAGTTCTGTCAGCGCGCGGGATCACTCTCGGCATGGAGCGAGCTGTACAAGAA	719
Db	913	CTGCTGGAGTTCTGTCAGCGCGCGGGATCACTCTCGGCATGGAGCGAGCTGTACAAGTA	971

Search completed: November 5, 2004, 16:57:35  
Job time : 110 secs

10/5/20

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 16:28:30 ; Search time 537 Seconds  
(without alignments)  
8522.344 Million cell updates/sec

Title: US-09-931-232-2

Perfect score: 850

Sequence: 1 atgggagcaagggcgagga.....taggatcaatgtgtagatgc 850

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubppna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubppna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubppna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubppna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubppna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubppna/PCTUS\_PUBCOMB.seq.\*
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- 8: /cgn2\_6/ptodata/2/pubppna/US08\_PUBCOMB.seq.\*
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- 10: /cgn2\_6/ptodata/2/pubppna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubppna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubppna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubppna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubppna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubppna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubppna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubppna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubppna/US11\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubppna/US11\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubppna/US60\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubppna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	850	9	US-09-931-232-2
2	850	100.0	4336	17	US-10-679-191A-1
3	850	100.0	4862	15	US-10-161-403-87
4	845	99.4	845	17	US-10-332-733-21
5	721.2	84.8	10417	14	US-10-152-040-28
6	720.6	84.8	6418	16	US-10-408-456-2
7	720	84.7	12789	16	US-10-666-778-9
8	719.4	84.6	8255	17	US-10-334-235-17
9	719.4	84.6	8528	14	US-10-239-804-11
10	719.2	84.6	5713	9	US-09-963-206B-5
11	719.2	84.6	5713	9	US-09-966-976A-5
12	719.2	84.6	5713	12	US-09-963-247A-5

13	719	84.6	8531	15	US-10-134-643-5	Sequence 5, Appli
14	719	84.6	8531	16	US-10-408-456-1	Sequence 1, Appli
15	719	84.6	8531	16	US-10-429-608A-2	Sequence 2, Appli
16	719	84.6	8531	16	US-10-716-725-2	Sequence 2, Appli
17	718.6	84.5	1190	11	US-09-927-876-98	Sequence 98, Appl
18	718.6	84.5	1190	16	US-10-360-149-98	Sequence 98, Appl
19	718.6	84.5	1190	16	US-10-457-047-98	Sequence 98, Appl
20	718.6	84.5	1377	15	US-10-204-724-1	Sequence 1, Appli
21	718.6	84.5	4151	16	US-10-421-285-15	Sequence 15, Appli
22	718.6	84.5	4733	10	US-09-797-496B-1	Sequence 1, Appli
23	718.6	84.5	4733	15	US-10-177-390-1	Sequence 1, Appli
24	718.6	84.5	4944	13	US-10-001-189-55	Sequence 55, Appli
25	718.6	84.5	4952	13	US-10-001-189-52	Sequence 52, Appli
26	718.6	84.5	7015	9	US-09-770-315-1	Sequence 1, Appli
27	718.6	84.5	9013	13	US-10-001-189-50	Sequence 50, Appli
28	718.6	84.5	9941	14	US-10-243-553-3	Sequence 3, Appli
29	718.6	84.5	9941	14	US-10-243-816-2	Sequence 2, Appli
30	718.6	84.5	9941	15	US-10-243-820-9	Sequence 9, Appli
31	718.6	84.5	9941	15	US-10-243-817-9	Sequence 9, Appli
32	718.6	84.5	9941	15	US-10-319-341-3	Sequence 3, Appli
33	718.6	84.5	14262	17	US-10-163-863A-9	Sequence 9, Appli
34	718.2	84.5	5162	10	US-09-815-981-13	Sequence 13, Appli
35	718.2	84.5	5162	10	US-09-815-979-13	Sequence 13, Appli
36	718.2	84.5	5162	15	US-10-235-119-13	Sequence 13, Appli
37	718.2	84.5	5162	15	US-10-161-403-26	Sequence 26, Appli
38	718.2	84.5	5162	15	US-10-086-745-13	Sequence 13, Appli
39	718.2	84.5	5162	15	US-10-428-653-13	Sequence 13, Appli
40	718	84.5	5100	10	US-09-954-483A-14	Sequence 14, Appli
41	718	84.5	5510	15	US-10-161-403-71	Sequence 71, Appli
42	718	84.5	5630	17	US-10-473-637-9	Sequence 9, Appli
43	718	84.5	6100	15	US-10-314-861-36	Sequence 36, Appli
44	718	84.5	6115	15	US-10-314-861-34	Sequence 34, Appli
45	718	84.5	6119	15	US-10-161-403-126	Sequence 126, App

#### ALIGNMENTS

RESULT 1  
US-09-931-232-2  
; Sequence 2, Application US/09931232  
; Publication No. US20020058274A1  
; GENERAL INFORMATION:  
; APPLICANT: Kain, Steve  
; TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins  
; FILE REFERENCE: CLON075CON  
; CURRENT APPLICATION NUMBER: US/09/931.232  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/364,946  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 09/191,233  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: 09/062,102  
; PRIOR FILING DATE: 1998-04-17  
; PRIOR APPLICATION NUMBER: 60/060,855  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 850  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence of the EGFP-MODC422\_461 fusion protein.  
US-09-931-232-2

Query Match 100.0%; Score 850; DB 9; Length 850;  
Best Local Similarity 100.0%; Pred. No. 7.4e-189;  
Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 4085 TACCTGAGCACCCAGTCCGCTGAGCAGAGACCCCAACGAGAGCGGATCACATGGTC 4144  
QY 661 CTGCTGGAGTTCTGAGCCGCCCGGGGATCACTTCGGGATGGAAGAGCTGTACAGAG 720  
Db 4145 CTGCTGGAGTTCTGAGCCGCCCGGGGATCACTTCGGGATGGAAGAGCTGTACAGAG 4204  
QY 721 CTTAGCCATGGCTTCCCGCGAGGTGGAGGAGCAGGATGATGGCAGCGTCCCATGCT 780  
Db 4205 CTTAGCCATGGCTTCCCGCGAGGTGGAGGAGCAGGATGATGGCAGCGTCCCATGCT 4264  
QY 781 TGTGCCAGGAGAGCGGGATGACCGTCAACCGTGCAGCGCTGTGCTTCTAGGATCAAT 840  
Db 4265 TGTGCCAGGAGAGCGGGATGACCGTCAACCGTGCAGCGCTGTGCTTCTAGGATCAAT 4324  
QY 841 GTGTAGATGC 850  
Db 4325 GTGTAGATGC 4334

## RESULT 3

US-10-161-403-87  
; Sequence 87, Application US/10161403  
; Publication No. US20030119104A1  
; GENERAL INFORMATION:  
; APPLICANT: Perkins, Edward  
; APPLICANT: Perez, Carl  
; APPLICANT: Lindenbaum, Michael  
; APPLICANT: Greene, Amy  
; APPLICANT: Leung, Josephine  
; APPLICANT: Fleming, Elena  
; APPLICANT: Stewart, Sandra  
; APPLICANT: Shellard, Joan  
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS  
; FILE REFERENCE: 24601-420  
; CURRENT APPLICATION NUMBER: US/10/161.403  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/294,758  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: 60/366,891  
; PRIOR FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 87  
; LENGTH: 4862  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pd2egfp-1N plasmid from Clontech  
US-10-161-403-87

Query Match 100.0%; Score 850; DB 15; Length 4862;  
Best Local Similarity 100.0%; Pred. No. 8.3e-189;  
Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGCCCATCTCCGTTCCGAGCTGGAC 60  
Db 679 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGCCCATCTCCGTTCCGAGCTGGAC 738  
QY 61 GGGCAGCTAAACGGGCCCAAGTTAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC 120  
Db 739 GGGCAGCTAAACGGGCCCAAGTTAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC 798  
QY 121 GGCAAGCTGACCTGAGTTTCATCTGCACCAACCGGGAAGCTGCCGTGCCCTGGCCGCCACC 180  
Db 799 GGCAAGCTGACCTGAGTTTCATCTGCACCAACCGGGAAGCTGCCGTGCCCTGGCCGCCACC 858  
QY 181 CTGCTGACCAACCTGACCTACGGCGTGCAGTGTTCAGCGCGTACCCCGACCATCAAG 240  
Db 859 CTGCTGACCAACCTGACCTACGGCGTGCAGTGTTCAGCGCGTACCCCGACCATCAAG 918  
QY 241 CAGCAGACTTCTTCAAGTCCCGCATGCCCGAAGGCTACCTCCAGGAGCGCAGCATCTTC 300  
Db 919 CAGCAGACTTCTTCAAGTCCCGCATGCCCGAAGGCTACCTCCAGGAGCGCAGCATCTTC 978

## RESULT 4

US-10-332-733-21  
; Sequence 21, Application US/10332733  
; Publication No. US20040106565A1  
; GENERAL INFORMATION:  
; APPLICANT: Margaret Odenthal and Diana Jung  
; TITLE OF INVENTION: Gene Expression, Genome Alteration And Reporter Expression  
; FILE REFERENCE: In Myofibroblasts And Myofibroblast-like Cells  
; CURRENT APPLICATION NUMBER: US/10/332,733  
; CURRENT FILING DATE: 2003-06-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 845  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence: EGFP  
US-10-332-733-21

Query Match 99.4%; Score 845; DB 17; Length 845;  
Best Local Similarity 100.0%; Pred. No. 1.1e-187;  
Matches 845; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGCCCATCTCCGTTCCGAGCTGGAC 60  
Db 1 ATGGTGAGCAAGGGCGAGGAGCTGTTCAACCGGGTGTGCCCATCTCCGTTCCGAGCTGGAC 60  
QY 61 GGGCAGCTAAACGGGCCCAAGTTAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC 120

Db	61	GGCGACGTAAACGGCCACAAGTTACGCTGTCGGCGAGGGGCGAGGGCGATGCGACCTAC	120
QY	121	GGCAAGCTGACCTCAAGTTTATCTGCACCAACGGCAAGCTGCCCGTGCCTTGGCCAC	180
Db	121	GGCAAGCTGACCTCAAGTTTATCTGCACCAACGGCAAGCTGCCCGTGCCTTGGCCAC	180
QY	181	CTGTGACCAACCTGACCTACGCTAGCGGTGAGTCTTTCAGCGGTACCCCGACACATGAAG	240
Db	181	CTGTGACCAACCTGACCTAGCGGTGAGTCTTTCAGCGGTACCCCGACACATGAAG	240
QY	241	CAGCAGCACTTCTCAAGTCCGCTACGCTGCGGAGGCTAGTCCAGGAGGCGACCATCTTC	300
Db	241	CAGCAGCACTTCTCAAGTCCGCTACGCTGCGGAGGCTAGTCCAGGAGGCGACCATCTTC	300
QY	301	TTCAAGGACGACGGCAACTACAAAGACCCGCGCGAGGTGAAGTTTCAGAGGCGACACCTTG	360
Db	301	TTCAAGGACGACGGCAACTACAAAGACCCGCGCGAGGTGAAGTTTCAGAGGCGACACCTTG	360
QY	361	GTGAACCGCATCGAGTGAAGGGCATTCGAATTCGAAGGAGGAGCGGCAACATCTCTGGGGAC	420
Db	361	GTGAACCGCATCGAGTGAAGGGCATTCGAATTCGAAGGAGGAGCGGCAACATCTCTGGGGAC	420
QY	421	AAAGCTGGAGTACAACTACAAAGCCCAACAGCTTATATCATGCGCAGCAAGCAGAGAAC	480
Db	421	AAAGCTGGAGTACAACTACAAAGCCCAACAGCTTATATCATGCGCAGCAAGCAGAGAAC	480
QY	481	GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCAAGCTGCGCTCGCC	540
Db	481	GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCAAGCTGCGCTCGCC	540
QY	541	GACCATACAGAGAACACCCCATCGGGAGCGGCGGCGGCTGCTGCTGCCGACACAC	600
Db	541	GACCATACAGAGAACACCCCATCGGGAGCGGCGGCGGCTGCTGCTGCCGACACAC	600
QY	601	TACCTGAGCAGCAGTCCGCTGAGCAAGACCCCAAGAGCGGCGGATCATATGCTC	660
Db	601	TACCTGAGCAGCAGTCCGCTGAGCAAGACCCCAAGAGCGGCGGATCATATGCTC	660
QY	661	CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGAGCAGCTGTACAAGAG	720
Db	661	CTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGAGCAGCTGTACAAGAG	720
QY	721	CTTAGCATGCTTCCGCGGAGGTGAGGAGCAGGATGATGCGACGCTGCCCATGCT	780
Db	721	CTTAGCATGCTTCCGCGGAGGTGAGGAGCAGGATGATGCGACGCTGCCCATGCT	780
QY	781	TGTGCCAGAGAGCGGATGAGCGCTACCCCTGACGCTGTGCTTCTGCTAGGATCAAT	840
Db	781	TGTGCCAGAGAGCGGATGAGCGCTACCCCTGACGCTGTGCTTCTGCTAGGATCAAT	840
QY	841	GTGTA 845	
Db	841	GTGTA 845	
RESULT 5			
US-10-152-040-28			
; Sequence 28, Application US/10152040			
; Publication No. US20030077251A1			
; GENERAL INFORMATION:			
; APPLICANT: ESCRIOU, NICOLAS			
; APPLICANT: VAN DER WERF, SYLVIE			
; APPLICANT: VIGNUZZI, MARCO			
; APPLICANT: GERBAUD, SYLVIE			
; TITLE OF INVENTION: REPLICONS DERIVED FROM POSITIVE STRAND RNA VIRUS			
; TITLE OF INVENTION: GENOMES USEFUL FOR THE PRODUCTION OF HETEROLOGOUS			
; TITLE OF INVENTION: PROTEINS			
; FILE REFERENCE: 03495.0229-00000			
; CURRENT APPLICATION NUMBER: US/10/152.040			
; CURRENT FILING DATE: 2002-06-27			
; PRIOR APPLICATION NUMBER: 60/292,515			
; PRIOR FILING DATE: 2001-05-23			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 28			
; LENGTH: 10417			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic			
; OTHER INFORMATION: Plasmid pm(DELTA)BB-GFP-IcmvNP			
US-10-152-040-28			
Query Match 84.8%; Score 721.2; DB 14; Length 10417;			
Best Local Similarity 97.6%; Pred. No. 9.9e-159;			
Matches 732; Conservative 0; Mismatches 18; Indels 0; Gaps 0;			
QY	1	ATGCTGAGCAAGGGGAGGAGCTGTTCACCGGGTGGTCCCATCTCTGCTCGAGCTGGAC	60
Db	743	ATGCTGAGCAAGGGGAGGAGCTGTTCACCGGGTGGTCCCATCTCTGCTCGAGCTGGAC	802
QY	61	GGCGACGTAAACGGCCACAAGTTTACGCTGTCGGCGAGGGGCGAGGGCGATGCGACCTAC	120
Db	803	GGCGACGTAAACGGCCACAAGTTTACGCTGTCGGCGAGGGGCGAGGGCGATGCGACCTAC	862
QY	121	GGCAAGCTGACCTCAAGTTTATCTGCACCAACGGCAAGCTGCCCGTGCCTTGGCCAC	180
Db	863	GGCAAGCTGACCTCAAGTTTATCTGCACCAACGGCAAGCTGCCCGTGCCTTGGCCAC	922
QY	181	CTGTGACCAACCTGACCTAGCGGTGAGTCTTTCAGCGGTACCCCGACACATGAAG	240
Db	923	CTGTGACCAACCTGACCTAGCGGTGAGTCTTTCAGCGGTACCCCGACACATGAAG	982
QY	241	CAGCAGCACTTCTCAAGTCCGCCCAACATCGAGGAGCGGCAAGCTGCGCTCTTC	300
Db	983	CAGCAGCACTTCTCAAGTCCGCCCAACATCGAGGAGCGGCAAGCTGCGCTCTTC	1042
QY	301	TTCAAGGACGACGGCAACTACAAAGACCCGCGCGAGGTGAAGTTTCAGAGGCGACACCTG	360
Db	1043	TTCAAGGACGACGGCAACTACAAAGACCCGCGCGAGGTGAAGTTTCAGAGGCGACACCTG	1102
QY	361	GTGAACCGCATCGAGTGAAGGGCATTCGAATTCGAAGGAGGCGGCAACATCTCTGGGGAC	420
Db	1103	GTGAACCGCATCGAGTGAAGGGCATTCGAATTCGAAGGAGGCGGCAACATCTCTGGGGAC	1162
QY	421	AAAGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGAGCAGCTGTACAAGAG	480
Db	1163	AAAGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGAGCAGCTGTACAAGAG	1222
QY	481	GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCAAGCTGCGCTCGCC	540
Db	1223	GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCAAGCTGCGCTCGCC	1282
QY	541	GACCATACAGAGAACACCCCATCGGGAGCGGCGGCGGCTGCTGCTGCCGACACAC	600
Db	1283	GACCATACAGAGAACACCCCATCGGGAGCGGCGGCGGCTGCTGCTGCCGACACAC	1342
QY	601	TACCTGAGCAGCAGTCCGCTGAGCAAGACCCCAAGAGCGGCGGATCATATGCTC	660
Db	1343	TACCTGAGCAGCAGTCCGCTGAGCAAGACCCCAAGAGCGGCGGATCATATGCTC	1402
QY	661	CTGCTGGAGTTCGTGACCGCGGAGGTGAGGAGCAGGATGATGCGACGCTGCCCATGCT	720
Db	1403	CTGCTGGAGTTCGTGACCGCGGAGGTGAGGAGCAGGATGATGCGACGCTGCCCATGCT	1462
QY	721	CTTAGCATGCTTCCGCGGAGGTGAGGAGCAGGATGATGCGACGCTGCCCATGCT	780
Db	1463	CTTAGCATGCTTCCGCGGAGGTGAGGAGCAGGATGATGCGACGCTGCCCATGCT	1492
RESULT 6			
US-10-408-456-2			
; Sequence 2, Application US/10408456			
; Publication No. US20040013648A1			
; GENERAL INFORMATION:			
; APPLICANT: Oxford Biomedica (UK) Limited			

APPLICANT: KINGSMAN, et al., Alan John  
TITLE OF INVENTION: Vector System  
FILE REFERENCE: 674523-2016  
CURRENT APPLICATION NUMBER: US/10/408,456  
PRIOR FILING DATE: 2003-04-08  
PRIOR APPLICATION NUMBER: PCT/GB01/04433  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 0024550.6  
PRIOR FILING DATE: 2000-10-06  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 6418  
TYPE: DNA  
ORGANISM: Equine Infectious Anemia Virus  
US-10-408-456-2

Query Match 84.8%; Score 720.6; DB 16; Length 6418;  
Best Local Similarity 96.8%; Pred. No. 1.3e-158;  
Matches 735; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 60  
Db |||||  
QY 2690 ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 2749  
Db |||||  
QY 61 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 120  
Db |||||  
QY 2750 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 2809  
Db |||||  
QY 121 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCACCGCGAGCTGCCGTGCCCTGGCCACCC 180  
Db |||||  
QY 2810 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCACCGCGAGCTGCCGTGCCCTGGCCACCC 2869  
Db |||||  
QY 181 CTCGTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 240  
Db |||||  
QY 2870 CTCGTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 2929  
Db |||||  
QY 241 CAGCAGCACTTCTTCAAGTCCGCCATGCGCGAGCTGAGTTCAGCGGCTACCCCGACCATGATGAG 300  
Db |||||  
QY 2930 CAGCAGCACTTCTTCAAGTCCGCCATGCGCGAGCTGAGTTCAGCGGCTACCCCGACCATGATGAG 2989  
Db |||||  
QY 301 TTCAGGACGACGCGCAACTACAAAGACCCGCGCGAGGTGAAAGTTCAGCGGCTACCCCGACCATGATGAG 360  
Db |||||  
QY 2990 TTCAGGACGACGCGCAACTACAAAGACCCGCGCGAGGTGAAAGTTCAGCGGCTACCCCGACCATGATGAG 3049  
Db |||||  
QY 361 GTGAACCCGATCGAGCTGAAAGGATCGACTTCAAGGAGGACGCGCAACATCTCTGGGGCAC 420  
Db |||||  
QY 3050 GTGAACCCGATCGAGCTGAAAGGATCGACTTCAAGGAGGACGCGCAACATCTCTGGGGCAC 3109  
Db |||||  
QY 421 AAGCTGGAGTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 480  
Db |||||  
QY 3110 AAGCTGGAGTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 3169  
Db |||||  
QY 481 GGCACTAAGGTGAATCTTCAAGTCCGCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 540  
Db |||||  
QY 3170 GGCACTAAGGTGAATCTTCAAGTCCGCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 3229  
Db |||||  
QY 541 GACCACTACAGGAGACACACCCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 600  
Db |||||  
QY 3230 GACCACTACAGGAGACACACCCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 3289  
Db |||||  
QY 601 TACCTGAGCACCAGTCCGCTGAGCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 660  
Db |||||  
QY 3290 TACCTGAGCACCAGTCCGCTGAGCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 3349  
Db |||||  
QY 661 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Db |||||  
QY 3350 CTGCTGGAGTTCGTGACCGCGCGCGGATCACTCTCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Db |||||  
QY 721 CTGAGCAGTGGCTTCCCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 759  
Db |||||  
QY 3410 AGCGCGCGGAGCTTAGAGTTCGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3448  
Db |||||

## RESULT 7

US-10-666-778-9/c  
Sequence 9, Application US/10666778  
Publication No. US20040064849A1  
GENERAL INFORMATION:  
APPLICANT: Goossens, Alain  
FILE OF INVENTION: Inze, Dirk  
TITLE OF INVENTION: PRODUCTION OF SECONDARY METABOLITES IN BIOLOGICAL CELLS  
FILE REFERENCE: DI/ABC/V082  
CURRENT APPLICATION NUMBER: US/10/666,778  
CURRENT FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: EP01201407.2  
PRIOR FILING DATE: 2001-04-18  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 12789  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: vector pK7WG2D  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (4772)..(4772)  
OTHER INFORMATION: n can be any base  
US-10-666-778-9

Query Match 84.7%; Score 720; DB 16; Length 12789;  
Best Local Similarity 100.0%; Pred. No. 1.9e-158;  
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 60  
Db |||||  
QY 5797 ATGGTGAGCAAGGGCGAGGAGTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 5738  
Db |||||  
QY 61 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 120  
Db |||||  
QY 5737 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 5678  
Db |||||  
QY 121 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 180  
Db |||||  
QY 5677 GCGCAGCTAAACGGCCACAAAGTTCAGCGTGTCCGGGAGGGCGAGGCGATGCCACCTAC 5618  
Db |||||  
QY 181 CTCGTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 240  
Db |||||  
QY 5617 CTCGTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 5558  
Db |||||  
QY 241 CAGCAGCACTTCTTCAAGTCCGCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 300  
Db |||||  
QY 5557 CAGCAGCACTTCTTCAAGTCCGCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 5498  
Db |||||  
QY 301 TTCAGGACGACGCGCAACTACAAAGACCCGCGCGAGGTGAAAGTTCGAGGGCGACACCCCTG 360  
Db |||||  
QY 5497 TTCAGGACGACGCGCAACTACAAAGACCCGCGCGAGGTGAAAGTTCGAGGGCGACACCCCTG 5438  
Db |||||  
QY 361 GTGAACCGCATCGAGCTGAAAGGCGATCGACTTCAAGGAGGACGCGCAACATCTCTGGGGCAC 420  
Db |||||  
QY 5437 GTGAACCGCATCGAGCTGAAAGGCGATCGACTTCAAGGAGGACGCGCAACATCTCTGGGGCAC 5378  
Db |||||  
QY 421 AAGCTGGAGTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 480  
Db |||||  
QY 5377 AAGCTGGAGTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 5318  
Db |||||  
QY 481 GGCACTAAGGTGAATCTTCAAGTCCGCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 540  
Db |||||  
QY 5317 GGCACTAAGGTGAATCTTCAAGTCCGCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 5258  
Db |||||  
QY 541 GACCACTACAGGAGACACCCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 600  
Db |||||  
QY 5257 GACCACTACAGGAGACACCCCATCGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGACGCGAGGAC 5198  
Db |||||



Qy	601	TACCTGAGCAACCAAGTCCGCCCTTGAGCAAGAGCCCAACAGAGAGCGGATCATCATGGTC	660
Db	5197	TACCTGAGCAACCAAGTCCGCCCTTGAGCAAGAGCCCAACAGAGAGCGGATCATCATGGTC	5138
Qy	661	CTGCTGAGAGTTCGTAGCCGCGCGGGATCACTCTCGGATGGACAGAGCTGTTCAGAGAG	720
Db	5137	CTGCTGAGAGTTCGTAGCCGCGCGGGATCACTCTCGGATGGACAGAGCTGTTCAGAGAG	5078

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RESULT 8
US-10-334-235-17
; Sequence 17, Application US/10334235
; Publication No. US20040134591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 8255
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nuc sequence of the
US-10-334-235-17

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Query Match	84.6%	Score 719.4	DB 17	Length 8255	
Best Local Similarity	97.2%	Prod. No. 2.6e-158			
Matches 732	Conservative	0	Mismatches 21	Indels 0	Gaps 0
QY	1	ATGTGTACCAAGGCGAGGAGCTGTTTACACCGGGTGTGCCCCATCTCTGTCTGCAGCTCGAC	60		
Db	2868	ATGTGTACCAAGGCGAGGAGCTGTTTACACCGGGTGTGCCCCATCTCTGTCTGCAGCTCGAC	2927		
QY	61	GGCGACGTAACCGGCCACAAGTTTACGCTGTCCGCGAGGCGGAGGGCGATGCCACCTTAC	120		
Db	2928	GGCGACGTAACCGGCCACAAGTTTACGCTGTCCGCGAGGCGGAGGGCGATGCCACCTTAC	2987		
QY	121	GGCAGCTTACCCCTGAAGTTTATCTGCACACCGCGACAGCTGCCGCTGCCCTGCCCCACC	180		
Db	2988	GGCAAGCTTACCCCTGAAGTTTATCTGCACACCGCGACAGCTGCCGCTGCCCTGCCCCACC	3047		
QY	181	CTCGTGACACACCTGACCTACGGCGTGAGTGCCTTACGCGCTACCCGACCAATGAAG	240		
Db	3048	CTCTGTACCAACCTGACCTACGGCGTGAGTGCCTTACGCGCTACCCGACCAATGAAG	3107		
QY	241	CAGCAGCATTTCTCAAGTCCGCCATGCCGAGGCTACGTTCCAGGAGCGCACCATCTTTC	300		
Db	3108	CAGCAGCATTTCTCAAGTCCGCCATGCCGAGGCTACGTTCCAGGAGCGCACCATCTTTC	3167		
QY	301	TTTCAAGGACGACGGCAAATTACAAGACCCGCGCGAGGTGAAGTTTCAGGGGGGACACCCCTG	360		
Db	3168	TTTCAAGGACGACGGCAAATTACAAGACCCGCGCGAGGTGAAGTTTCAGGGGGGACACCCCTG	3227		
QY	361	GTGAACCGCATCGAGCTGAAGGCGATCGACTTTCAGGAGGACGGCAATCTCTGGGGCAC	420		
Db	3228	GTGAACCGCATCGAGCTGAAGGCGATCGACTTTCAGGAGGACGGCAATCTCTGGGGCAC	3287		

Qy	421	AGCTGGAGTACAACTCTACACAGCCACRAGCTCTATATCATGGCCGACAAAGCAGAAGAAC	480
Db	3288	AACTGGAGTACAACTACACAGCCACRAGCCAAACGCTCTATATCATGGCCGACRAGCAGAAGAAC	3347
Qy	481	GGCATCAAGGTGAACCTTCAAGATCCGCCCAACAATCGAGGACGGCAGCTGTACAGTCGGCC	540
Db	3348	GGCATCAAGGTGAACCTTCAAGATCCGCCCAACAATCGAGGACGGCAGCTGTACAGTCGGCC	3407
Qy	541	GACCACTACAGCAGACRACCCCACTGGCGACGGCCCGTGTCTGTGCCCGGACAAACCCAC	600
Db	3408	GACCACTACAGCAGACRACCCCACTGGCGACGGCCCGTGTCTGTGCCCGGACAAACCCAC	3467
Qy	601	TACCTGAGCACCCAGTCCGCCCTTGAGCAAGAAGACCCCAACGAGAAGCGCGATCATATGGTC	660
Db	3468	TACCTGAGCACCCAGTCCGCCCTTGAGCAAGAAGACCCCAACGAGAAGCGCGATCATATGGTC	3527
Qy	661	CTACTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGACACGAGCTGTGTACAAGAAG	720
Db	3528	CTACTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGACACGAGCTGTGTACAAGTAA	3587
Qy	721	CTTAGCCATGGCTTCCGCCGCGAGGTGGAGGAG	753
Db	3588	AGCGGCGCGCACTCTAGAGTCGACCTCGAGGGG	3620

RESULT	9
US-10-23	
Sequenc	:
Public	:
GENERAL	:
APPLI	:
APPLI	:
APPLI	:
TITLE	:
FILE	:
CURRE	:
CURRE	:
PRIOR	:
PRIOR	:
PRIOR	:
PRIOR	:
NUMBB	:
SQW	:
SEQ II	:
LENG	:
TYPE	:
ORGAN	:
FEAT	:
OTHER	:
OTHER	:
US-10-23	

Query Match	84.6%	Score 719.4	DB 14	Length 8528
Best Local Similarity	97.2%	Pred. No. 2.6e-158		
Matches 732	Conservative 0	Mismatches 21	Indels 0	Gaps 0
QY	1	ATGTGTGACGAGCGGAGGAGCTTTTCACCGGGGTGTGCCCATCTCTGTGTCGAGCTGGAC	60	
DB	2868	ATGTTTGACGACGAGCGGAGGAGCTTTTCACCGGGGTGTGCCCATCTCTGTGTCGAGCTGGAC	2927	
QY	61	GGCGACGCTAAACGGCCCAAGATTTCAGCGGTTCGGCGGAGGCGGCGATGCCACTTAC	120	
DB	2928	GGCGACGCTAAACGGCCCAAGATTTCAGCGGTTCGGCGGAGGCGGCGATGCCACTTAC	2987	
QY	121	GGCAGCTGACCCCTGAAGTTTCATCTGCACCAACCGGCAAGCTGCCCGTGCCCTGCGCCCAACC	180	
DB	2988	GGCAGCTGACCCCTGAAGTTTCATCTGCACCAACCGGCAAGCTGCCCGTGCCCTGCGCCCAACC	3047	
QY	181	CTCCTGACCACCCCTGACCTACGGCGTGGAGTGTTCACGCGCTTACCCCGACCAATGAAG	240	
DB	3048	CTCGTGACCACTTACCTGACCTACGGCGTGGAGTGTTCACGCGCTTACCCCGACCAATGAAG	3107	



Query Match 84.6%; Score 719.2; DB 9; Length 5713;  
Best Local Similarity 98.9%; Pred. No. 2.8e-158;  
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 60  
2150 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 2209  
61 GGGGACGTAAACGGCCACCAAGTTACGGGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120  
2210 GGGGACGTAAACGGCCACCAAGTTACGGGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2269  
121 GGCAGCTGACCTGACCTGAAAGTTCTGTCACCCGCGCAAGCTGCCCTGCCCTGCCCTGCC 180  
2270 GGCAGCTGACCTGACCTGAAAGTTCTGTCACCCGCGCAAGCTGCCCTGCCCTGCCCTGCC 2329  
181 CTCGTGACCAACCGCTGACCTGACCGCGTGCAGTGTTCAGCGCTTACCCCGGACCAATGAAG 240  
2330 CTCGTGACCAACCGCTGACCTGACCGCGTGCAGTGTTCAGCGCTTACCCCGGACCAATGAAG 2389  
241 CAGCAGCTTCTTCAAGTCCGCGCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTTC 300  
2390 CAGCAGCTTCTTCAAGTCCGCGCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTTC 2449  
301 TTCAAGGACGACCGCAACTACAGACCCGCGCGAGGTCAAAGTTCCAGGCGCGACACCCCTG 360  
2450 TTCAAGGACGACCGCAACTACAGACCCGCGCGAGGTCAAAGTTCCAGGCGCGACACCCCTG 2509  
361 GTGAACCGCATCGAGTGAAGGGCATCGATTCAAGGAGCGGCAACATCTCTGGGGCAC 420  
2510 GTGAACCGCATCGAGTGAAGGGCATCGATTCAAGGAGCGGCAACATCTCTGGGGCAC 2569  
421 AAGCTGAGGTACAACTACAGCGCAACAGCTTATATCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTC 480  
2570 AAGCTGAGGTACAACTACAGCGCAACAGCTTATATCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTC 2629  
481 GGCATCAAGGTGAACCTTCAAGATCCGCGCAACATCGAGGAGCGGCGAGCTCGCTCGCC 540  
2630 GGCATCAAGGTGAACCTTCAAGATCCGCGCAACATCGAGGAGCGGCGAGCTCGCTCGCC 2689  
541 GACCACTACGAGCAAGACCCCGCATCGGGGAGCGGCGCGCTGTCTGCTGCCGAGCAACAC 600  
2690 GACCACTACGAGCAAGACCCCGCATCGGGGAGCGGCGCGCTGTCTGCTGCCGAGCAACAC 2749  
721 CTTAGCCATGGC 732  
2870 TTGGAGGTGGC 2881

Query Match 84.6%; Score 719.2; DB 12; Length 5713;  
Best Local Similarity 98.9%; Pred. No. 2.8e-158;  
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 60  
2150 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 2209  
61 GGGGACGTAAACGGCCACCAAGTTACGGGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120  
2210 GGGGACGTAAACGGCCACCAAGTTACGGGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2269  
121 GGCAGCTGACCTGACCTGAAAGTTCTGTCACCCGCGCAAGCTGCCCTGCCCTGCCCTGCC 180  
2270 GGCAGCTGACCTGACCTGAAAGTTCTGTCACCCGCGCAAGCTGCCCTGCCCTGCCCTGCC 2329  
181 CTCGTGACCAACCGCTGACCTGACCGCGTGCAGTGTTCAGCGCTTACCCCGGACCAATGAAG 240  
2330 CTCGTGACCAACCGCTGACCTGACCGCGTGCAGTGTTCAGCGCTTACCCCGGACCAATGAAG 2389  
241 CAGCAGCTTCTTCAAGTCCGCGCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTTC 300  
2390 CAGCAGCTTCTTCAAGTCCGCGCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTTC 2449  
301 TTCAAGGACGACCGCAACTACAGACCCGCGCGAGGTCAAAGTTCCAGGCGCGACACCCCTG 360  
2450 TTCAAGGACGACCGCAACTACAGACCCGCGCGAGGTCAAAGTTCCAGGCGCGACACCCCTG 2509  
361 GTGAACCGCATCGAGTGAAGGGCATCGATTCAAGGAGCGGCAACATCTCTGGGGCAC 420  
2510 GTGAACCGCATCGAGTGAAGGGCATCGATTCAAGGAGCGGCAACATCTCTGGGGCAC 2569  
421 AAGCTGAGGTACAACTACAGCGCAACAGCTTATATCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTC 480  
2570 AAGCTGAGGTACAACTACAGCGCAACAGCTTATATCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTC 2629  
481 GGCATCAAGGTGAACCTTCAAGATCCGCGCAACATCGAGGAGCGGCGAGCTCGCTCGCC 540  
2630 GGCATCAAGGTGAACCTTCAAGATCCGCGCAACATCGAGGAGCGGCGAGCTCGCTCGCC 2689  
541 GACCACTACGAGCAAGACCCCGCATCGGGGAGCGGCGCGCTGTCTGCTGCCGAGCAACAC 600  
2690 GACCACTACGAGCAAGACCCCGCATCGGGGAGCGGCGCGCTGTCTGCTGCCGAGCAACAC 2749  
721 CTTAGCCATGGC 732  
2870 TTGGAGGTGGC 2881

Query Match 84.6%; Score 719.2; DB 9; Length 5713;  
Best Local Similarity 98.9%; Pred. No. 2.8e-158;  
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 60  
2150 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 2209  
61 GGGGACGTAAACGGCCACCAAGTTACGGGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120  
2210 GGGGACGTAAACGGCCACCAAGTTACGGGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2269  
121 GGCAGCTGACCTGACCTGAAAGTTCTGTCACCCGCGCAAGCTGCCCTGCCCTGCCCTGCC 180  
2270 GGCAGCTGACCTGACCTGAAAGTTCTGTCACCCGCGCAAGCTGCCCTGCCCTGCCCTGCC 2329  
181 CTCGTGACCAACCGCTGACCTGACCGCGTGCAGTGTTCAGCGCTTACCCCGGACCAATGAAG 240  
2330 CTCGTGACCAACCGCTGACCTGACCGCGTGCAGTGTTCAGCGCTTACCCCGGACCAATGAAG 2389  
241 CAGCAGCTTCTTCAAGTCCGCGCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTTC 300  
2390 CAGCAGCTTCTTCAAGTCCGCGCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTTC 2449  
301 TTCAAGGACGACCGCAACTACAGACCCGCGCGAGGTCAAAGTTCCAGGCGCGACACCCCTG 360  
2450 TTCAAGGACGACCGCAACTACAGACCCGCGCGAGGTCAAAGTTCCAGGCGCGACACCCCTG 2509  
361 GTGAACCGCATCGAGTGAAGGGCATCGATTCAAGGAGCGGCAACATCTCTGGGGCAC 420  
2510 GTGAACCGCATCGAGTGAAGGGCATCGATTCAAGGAGCGGCAACATCTCTGGGGCAC 2569  
421 AAGCTGAGGTACAACTACAGCGCAACAGCTTATATCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTC 480  
2570 AAGCTGAGGTACAACTACAGCGCAACAGCTTATATCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTC 2629  
481 GGCATCAAGGTGAACCTTCAAGATCCGCGCAACATCGAGGAGCGGCGAGCTCGCTCGCC 540  
2630 GGCATCAAGGTGAACCTTCAAGATCCGCGCAACATCGAGGAGCGGCGAGCTCGCTCGCC 2689  
541 GACCACTACGAGCAAGACCCCGCATCGGGGAGCGGCGCGCTGTCTGCTGCCGAGCAACAC 600  
2690 GACCACTACGAGCAAGACCCCGCATCGGGGAGCGGCGCGCTGTCTGCTGCCGAGCAACAC 2749  
601 TACCTGAGCACCCAGTCCGCGCTGAGCAAGACCCCAACGAGAGCGCGCATCATGGTC 660  
2750 TACCTGAGCACCCAGTCCGCGCTGAGCAAGACCCCAACGAGAGCGCGCATCATGGTC 2809  
661 CTGCTGAGTTCGTGACCGCGCGGGATCACTCTCGGCAATGAGCGAGCTGTACAAGAG 720  
2810 CTGCTGAGTTCGTGACCGCGCGGGATCACTCTCGGCAATGAGCGAGCTGTACAAGAG 2869  
721 CTTAGCCATGGC 732  
2870 TTGGAGGTGGC 2881

Query Match 84.6%; Score 719.2; DB 12; Length 5713;  
Best Local Similarity 98.9%; Pred. No. 2.8e-158;  
Matches 724; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
1 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 60  
2150 ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTCCCATCTCGTGTGAGCTGGAC 2209  
61 GGGGACGTAAACGGCCACCAAGTTACGGGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 120  
2210 GGGGACGTAAACGGCCACCAAGTTACGGGTGTCCGGCGAGGGCGAGGGCGATGCCACTAC 2269  
121 GGCAGCTGACCTGACCTGAAAGTTCTGTCACCCGCGCAAGCTGCCCTGCCCTGCCCTGCC 180  
2270 GGCAGCTGACCTGACCTGAAAGTTCTGTCACCCGCGCAAGCTGCCCTGCCCTGCCCTGCC 2329  
181 CTCGTGACCAACCGCTGACCTGACCGCGTGCAGTGTTCAGCGCTTACCCCGGACCAATGAAG 240  
2330 CTCGTGACCAACCGCTGACCTGACCGCGTGCAGTGTTCAGCGCTTACCCCGGACCAATGAAG 2389  
241 CAGCAGCTTCTTCAAGTCCGCGCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTTC 300  
2390 CAGCAGCTTCTTCAAGTCCGCGCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTTC 2449  
301 TTCAAGGACGACCGCAACTACAGACCCGCGCGAGGTCAAAGTTCCAGGCGCGACACCCCTG 360  
2450 TTCAAGGACGACCGCAACTACAGACCCGCGCGAGGTCAAAGTTCCAGGCGCGACACCCCTG 2509  
361 GTGAACCGCATCGAGTGAAGGGCATCGATTCAAGGAGCGGCAACATCTCTGGGGCAC 420  
2510 GTGAACCGCATCGAGTGAAGGGCATCGATTCAAGGAGCGGCAACATCTCTGGGGCAC 2569  
421 AAGCTGAGGTACAACTACAGCGCAACAGCTTATATCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTC 480  
2570 AAGCTGAGGTACAACTACAGCGCAACAGCTTATATCATGCGCGAGGCTAGTCCAGGAGCGCAATCTTC 2629  
481 GGCATCAAGGTGAACCTTCAAGATCCGCGCAACATCGAGGAGCGGCGAGCTCGCTCGCC 540  
2630 GGCATCAAGGTGAACCTTCAAGATCCGCGCAACATCGAGGAGCGGCGAGCTCGCTCGCC 2689  
541 GACCACTACGAGCAAGACCCCGCATCGGGGAGCGGCGCGCTGTCTGCTGCCGAGCAACAC 600  
2690 GACCACTACGAGCAAGACCCCGCATCGGGGAGCGGCGCGCTGTCTGCTGCCGAGCAACAC 2749  
601 TACCTGAGCACCCAGTCCGCGCTGAGCAAGACCCCAACGAGAGCGCGCATCATGGTC 660  
2750 TACCTGAGCACCCAGTCCGCGCTGAGCAAGACCCCAACGAGAGCGCGCATCATGGTC 2809  
661 CTGCTGAGTTCGTGACCGCGCGGGATCACTCTCGGCAATGAGCGAGCTGTACAAGAG 720  
2810 CTGCTGAGTTCGTGACCGCGCGGGATCACTCTCGGCAATGAGCGAGCTGTACAAGAG 2869  
721 CTTAGCCATGGC 732  
2870 TTGGAGGTGGC 2881

RESULT 13  
US-10-134-643-5  
; Sequence 5, Application US/10134643  
; Publication No. US20030113898A1  
; GENERAL INFORMATION:  
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and IgE Syn  
; TITLE OF INVENTION: Secretion and Switch Rearrangement  
; FILE REFERENCE: A-66038-1/RMS/JUD/DLR  
; CURRENT APPLICATION NUMBER: US/09/963,247A  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/076,624

```
; APPLICANT: OLSEN, JOHN C.
; APPLICANT: MITROPHANOUS, KYRIACOS ANDREOU
; APPLICANT: ROHL, JONATHAN
; APPLICANT: KINGSMAN, ALAN JOHN
; APPLICANT: ELLARD, FIONA MARGARET
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGH TITRE VECTORS AND
; TITLE OF INVENTION: COMPOSITIONS USED IN SUCH METHODS
; FILE REFERENCE: 078883-0148
; CURRENT APPLICATION NUMBER: US/10/134,643
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/287,048
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 8531
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleic acid pONY8G, vector genome plasmid
US-10-134-643-5

Query Match      84.6%; Score 719; DB 15; Length 8531;
Best Local Similarity 97.3%; Pred. No. 3.2e-158;
Matches 731; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGTGCCCATCTCTGTGAGCTGGAC 60
Db 2690 ATGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGTGCCCATCTCTGTGAGCTGGAC 2749

Qy 61 GGCAGCTTAACGGCCCAAGTTTACCGGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC 120
Db 2750 GGCAGCTTAACGGCCCAAGTTTACCGGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC 2809

Qy 121 GGCAGCTTAACGGCCCAAGTTTACCGGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC 180
Db 2810 GGCAGCTTAACGGCCCAAGTTTACCGGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC 2869

Qy 181 CTCGTGACCAACCTGACCTACGGGTGAGTTCAGCCGCTTACCGGCTACCGGACCATGAAG 240
Db 2870 CTCGTGACCAACCTGACCTACGGGTGAGTTCAGCCGCTTACCGGCTACCGGACCATGAAG 2929

Qy 241 CAGCAGCACTTCTTCAAGTCCGCCATGCCGAGGCTACGTCAGGAGCGGACCATCTTC 300
Db 2930 CAGCAGCACTTCTTCAAGTCCGCCATGCCGAGGCTACGTCAGGAGCGGACCATCTTC 2989

Qy 301 TTCAAGCGCATCGAGCTGAAGGATCGACTTCAAGGAGCGGCAACATCCTGGGGCAC 420
Db 3050 TTCAAGCGCATCGAGCTGAAGGATCGACTTCAAGGAGCGGCAACATCCTGGGGCAC 3109

Qy 421 AAGCTGGAGTACACTCAACAGCCCAACATCGAGGAGCGGCGAGGTGAGTTCAGGAGG 480
Db 3110 AAGCTGGAGTACACTCAACAGCCCAACATCGAGGAGCGGCGAGGTGAGTTCAGGAGG 3169

Qy 481 GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCGAGGTGAGTTCAGGAGG 540
Db 3170 GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCGAGGTGAGTTCAGGAGG 3229

Qy 541 GGCATCAAGGTGAATCTCAAGATCCGCCCAACATCGAGGAGCGGCGAGGTGAGTTCAGGAGG 600
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## RESULT 15

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; Sequence 2, Application US/10429608A  
; Publication No. US20040071675A1  
; GENERAL INFORMATION:  
; APPLICANT: MAZARAKIS, NICHOLAS  
; APPLICANT: AZZOUZ, MINOUN  
; TITLE OF INVENTION: VECTOR SYSTEM  
; FILE REFERENCE: 674523-2017  
; CURRENT APPLICATION NUMBER: US/10/429,608A  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: PCT/GB01/04866  
; PRIOR FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: GB 0122238.9  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: GB 0102339.9  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: GB 0026943.1  
; PRIOR FILING DATE: 2000-11-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 8531  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: nucleotide construct pONY8G sequence  
US-10-429-608A-2

Query Match 84.6%; Score 719; DB 16; Length 8531;  
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